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COVID-19 AI STRUCTURAL MODEL TO MONITOR THE MULTIPLICATIVE NATURE OF COVID-19 INFECTIONS

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ABSTRACT: In the present COVID-19 situation, it poses a danger to a person's life because of organ infection and other health problems. It is mandatory to research work to find a better COVID-19 infection diagnosis method through scans and contact tracing through the AI method. In this, a novel AI structural model is intended to identify the infection features in the respective regions of human being availability, which makes the infection monitoring easier to identify an infected and non-infected human being from the population identified. The method used for monitoring the multiplicative nature of Coronavirus infections is through contact feature tracing and infection confirmation status and confirms the Coronavirus cases from scans and feature analysis to include real-time contact tracking from the same region and distant regions, providing an efficient method to track the infection spread. The anticipated model is used to forecast coronavirus transmission using feature forecasting data. The performance assessment is compared based on the outcomes of the suggested model and shows an enhanced COVID-19 diagnostic model.

INTRODUCTION: In the context of global turmoil, a new coronavirus illness (COVID-19) has developed that is harming individuals' lives and killing many. A worldwide health catastrophe is being brought on by the terrible effects this epidemic has on businesses and cultures throughout the globe. AI method has sent significant waves through recovery administrations, at every opportunity to provide current communication over time, AI experts will replace human experts after. Artificial intelligence's advantages lead to excessive sensitivity and specificity in the determination and reporting rate.

Artificial intelligence has made significant progress in predictive learning models of the clinical care system in recent years. Since, the diagnosis of the maximum number of public contaminated with coronavirus, if the human being has pneumonia, in the analysis, x-rays may be useful and assessment of the course of the disease. Calculated Chest Computed tomography (CT) screening at the initial process of an affected person increased sensitivity and was even confirmed as showing low or lower positive Coronavirus infection cases.

CT scans provide a lot more thorough view of the patient's condition than traditional X-rays, and this particular information may be utilized to determine if the issue is scientific. This is a significant bottleneck for the execution of this study effort, e.g., the right because of the volume and the real problem area. For these reasons, various feature methodologies have been proposed, mostly based on prediction methods for screening for

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coronavirus in computed tomography. When a deadly disease spreads freely in a population, it spreads at random. Here's why the diversity of infections increases exponentially over time and follows a nearly random distribution curve characteristic of the case. Estimated distribution of random infections in each area management measures was introduced, in addition to the population, a map of human social behavior (contact rate) was made by density and demographics. In this work, we recommend a structural model for the infection unfold which provides the effect of each of the measures imposed globally in disrupting publicity and reducing the transmission of the pandemic at a level of contamination through the human being.

The Rest of this Work is Presented: The most recent research on the proposed in this study perspective is compiled in Section 2. The recommended model is presented in Section 3. After that, we offer the assessment techniques in Section 4 and conclude this work with future directions in Section 5.

Previous Works: The COVID-19 image categorization framework is the only support for a deep learning model¹. The COVID-19 infection is detected in this study using X-rays. In², a different Coronavirus image evaluation system that is mostly based on deep learning has been suggested, and this study also employs X-rays for classification. This model, known as COVID-Net, has been used to analyze a significant number of X-ray pictures and has shown encouraging results. Comparable method *i.e.* in³ a category approach of X-ray imaging based entirely on deep learning, is proposed, which is referred to as Dark Covid Net. This article proposes a mechanism to detect a fully infected location based on a heat map. To automate the analysis approach of the Coronavirus illness, a new completely computerized image category structure that is mostly based on X-rays is presented in⁴. This project, which goes by the name COVID diagnosis-Net, is mostly built on the deep network Bayes-SqueezeNet. The authors of⁵ described a method for remotely controlling the usage of AI tools that are impacted by the coronavirus, mostly based on self-isolation and symptomatic therapy. The authors in⁶ emphasized the importance of computed tomography (CT)

characterization of COVID-19, which may be available in stages. Meanwhile, the authors of⁷ appeared in six assigned studies that identified the medicinal properties of COVID-19. The authors of⁸ reported a novel computational method for COVID-19 identification utilizing CXR images. The simulation is known as "DarkCovidNet." A deep CNN model was presented to identify a Coronavirus instance based on X-ray pictures⁹. The COVID-Net model is freely available and open source. To identify between any Coronavirus and non-Coronavirus CT images, several deep-learning algorithms were developed¹⁰. In¹¹, a hybrid AI model that combines epidemic versions (AI) of infected tools, NLP, and deep learning was developed to forecast the rate of Coronavirus infection.

As indicated in¹² and¹³, these modes have been utilized to correctly forecast instances of SARS and Ebola virus infection using differential equations to depict the connection between I, S and R. The taxonomy of coronavirus, nevertheless, is anticipated by Randhawa *et al.*¹⁴ to be primarily based on an unmatched ML technique¹⁵, the usage of genetic markers, and a decision tree methodology.

Various deep learning architectures now use a convolutional neural network, including COVID-Net¹⁶, DarkNet¹⁷, CovidX-net¹⁸, CheXnet¹⁹, COVID-SDnet²⁰ and pre-trained CNNs^{21, 22, 23-25} were done to identify coronavirus utilizing viral pneumonia and chest X-rays. The patient's lungs manage the severity of the virus by using CT scans to identify underlying clinical disorders that may be a factor²⁶. One of the foundational machine learning programs may be found in the healthcare system. It is utilized to identify any condition identified by clinical imaging, including lung infections, cancer, tumors, and injuries²⁷. Unsupervised learning employs unlabeled or unknown data, requiring more analysis than supervised learning. Without human assistance, it autonomously assesses options and spots patterns²⁸. Many COVID-19 detection methods exist in addition to conventional identification techniques. Chest X-rays (CXR) and computed tomography are the two most often used clinical imaging modalities for diagnosing lung infections^{29, 30}. While CT scans are commonly used to diagnose Coronavirus

^{31, 32}, cost ³³ and radiation exposure are important factors. In addition, high scan closeness has been observed in chest CT scans ^{34, 35} and radiographs show Coronavirus-related image markers ³⁶. Because of their widespread accessibility and low radiation, CXR pictures are preferable over CT scans.

Proposed Model: In the proposed solution for detecting Coronavirus, AI structural model is used for analyzing the spreading information of human beings. The diagnosis information is analyzed by a healthcare person for contact and infection spreading based on the distance between human beings. The diagnosis information is feature analyzed from scan reports and contact tracing to implement this. Through contact feature tracing, a human being within a social environment is considered in four ways for implementation; a) with a high probable infection staying for a longer duration in the same location and causing the infection to spread; b) with a low probable infection staying for a shorter duration in the same location and causing the infection to spread; c) with no probable infection staying for a longer duration in the same location and causing the no infection to spread; d) with moderate probable infection staying for an average duration in the same location and causing the infection to spread; and e) combination of above-mentioned scenarios. From social contact feature tracing, knowledge of infection spread helps the proposed model to analyze infected human beings located in the distant region, which increases the accuracy of the anticipated model to analyze the probability of contact tracing within the region and distant regions. The proposed model framework is integrated in the same region by analyzing the spreading within the same infected and non-infected human beings. The diagnosed features are used in distant regions to build a new model from the regions learned through diagnosing and distinguishing infected and non-infected human beings. **Fig. 1** illustrates the proposed model framework of the Coronavirus contact tracing system. At the diagnosis stage, every feature is analyzed for:

- ❖ Normal infected symptoms with it infection rates.
- ❖ Confirmed infected symptoms of an individual human being.

The human being showing highly infected feature symptoms at the severe stage was identified. At the moderate stage, the human being is showing moderate infected feature symptoms, which were identified because of contact with the infected human being based on the regions of contact tracing. At the mild stage, the human being showing a mildly infected feature symptom was identified to quarantine and isolate the human being from other people to avoid infection spreading.

Flowchart: **Fig. 1** shows the Coronavirus symptoms feature detection framework using AI and machine learning for abnormal and normal identification. Diagnosis features were extracted, and pooling was performed with the classification method by analyzing the region of the diagnosis region and reducing the feature computation time. The proposed model analyzed the diagnosis features in multi-domain, including time-frequency domains.

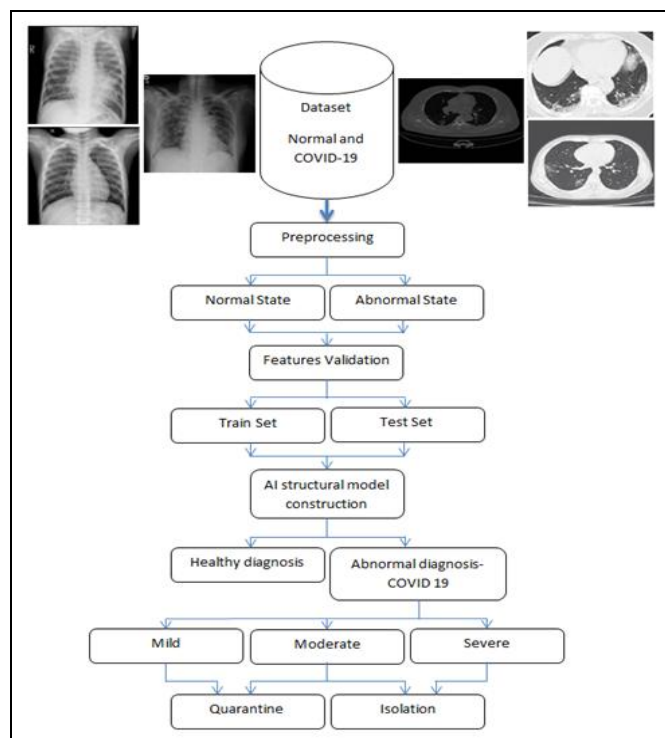


FIG. 1: FLOWCHART OF THE PROPOSED MODEL FRAMEWORK FOR CORONAVIRUS DIAGNOSIS DETECTION

Algorithm: Algorithm 1 outlines the analysis of the proposed multiplicative nature of coronavirus tracing. The proposed scheme provides a structural model method, where each contact in the model is a

human being with coronavirus status providing the diagnosis status:

- Location of infection analysis i.e., the geographical place of spread represented as (a,b), provided in the time.
- Changes in symptoms infection analysis i.e., daily estimated analysis represented as (p,q), provided in scan reports.

Point Sh1 in each S1 represents a human being and point Sh2 in each S2 represents another human being. If Sh1 is infected and between Sh1 and Sh2, the distance reduces, and the possibility of infection spread is available. The proposed algorithm can estimate the distances and analyze the infection status based on contact between Sh1 and Sh2.

If Sh1 is infected and the system identifies it as Identified Feature, then the possible infection status is provided with the diagnosis status, including:

- Contact Feature Tracing i.e., identification of infection progression through contact, provided in infection analysis.
- Infection confirm status, i.e., information from the scan and visual features through infection diagnosis status, provided in contact analysis.

The contact feature tracing between Sh1 and Sh2 distance contact for infection information is analyzed. The feature tracing variable has a complete scan report analysis of active infection cases and current infection status with high potential risk infection cases, which are identified

through infection confirmation status. Infection confirmation status is an approach implemented in this paper to analyze the specific duration of time; the infected Sh1 is nearer to Sh2 and the distance between Sh1 and Sh2. This creates a contract feature tracing, where Sh1 as an infected human being is maintained with infection confirmed status as positive. In infection confirm status based on Contact Feature Tracing, the human being scan analysis is categorized as 1) Positive-Confirmed-coronavirus infection case, 2) Negative-Confirmed-coronavirus infection case, and 3) Quarantine-Confirmed-coronavirus infection case.

These three sets represent scan diagnose status for feature Tracing through infection transmission between identified human beings, by analyzing the infection similarities of each infected human being identified as a Positive-Confirmed-coronavirus infection case or Quarantine-Confirmed-coronavirus infection case. Based on the Contact Feature Tracing, reducing the distance between human beings, which periodically changes, updates the infection confirm status between human beings. The model used in the proposed work uses a dynamic model analysis, having a distance theoretical model where the progressive infection history of each human being at all the time instants are traced using particular location and distance order. These model features are updated at specific time frames, which results in accurate infection spread analysis for better infection spread control optimization.

Algorithm 1: The pseudo-code of AI Structural Model construction

Input:	Human being population size N The social distance between human beings Social _{Dist} Infection symptom status Sym _{status} Maximum number of infection estimation repetition rate T
Output:	Best Infection Confirmation Status InfConf _{status} Infected and non-infected contact duration INIDur _{contact} Best Infection Spread Status Inf Spr _{status} Contact Duration Status ConDur _{status}
Initiate human being population analysis in a zone H _i (i=1,2,..., N)	
Begin	
t=0	
while t<T do	
for i=1:N do	
/** Find infected human being in the zone or outside the zone	
INIDur _{contact} = H _i > Social _{Dist}	
ConDur _{status} = Sym _{status} >INIDur _{contact}	
InfConf _{status} = Social _{Dist} > ConDur _{status}	
InfSpr _{status} = InfConf _{status} > Sym _{status}	

```

Update the InfConfstatus, fitness;
/** Find human being is positive or negative
if SocialDist<Symstatus and INIDurcontact> T
then INIDurcontact is positive
end
if SocialDist> Symstatus and INIDurcontact< T
then INIDurcontact is negative
End

/** Find infected human being status to quarantine or isolation requirements
if SocialDist< Symstatus then
for all Hi> SocialDist do
if Symstatus> ConDurstatus then
if ConDurstatus> T
then INIDurcontact is positive
end
end
if Symstatus< ConDurstatus then
if ConDurstatus< T and InfConfstatus< ConDurstatus
then INIDurcontact is negative
End
End
End
End

/** Predict infected human being confirmation status in spreading
for each Hi do
InfConfstatus = SocialDist> ConDurstatus
InfSprstatus = InfConfstatus> Symstatus
T=t+1
return Inf Confstatus, fitness;
end loop
    
```

RESULTS AND DISCUSSIONS: The proposed model simulated its experiments in a Matlab environment. The simulation is analyzed in a region of around 500m distance with a population density of 50 to 70 human beings, with each human being having 50: 30: 20 ratios of infected, moderate-infected, and not-infected symptoms. A flag is established in matrix form for identification in the simulation environment as [I: M: N],

represented for Infected: Moderate-Infected: Not-Infected. Symptom for a human being in the designated region is estimated using the proposed model.

Dataset Evaluation: Table 1 shows the datasets used, and the description of the dataset portioning is shown in Table 2.

TABLE 1: X-RAY AND CT-SCAN FOR CORONAVIRUS CASES AND NORMAL CASES

Type	Dataset Name	Feature Fitting Data	Coronavirus	Non- coronavirus
X-ray	Normal and coronavirus X-ray images	Ffit_1	1011	1308
	Data augmented coronavirus X-ray images	Ffit_2	1392	789
	coronavirus X-ray images	Ffit_3	223	232
CT-scan	Normal and coronavirus CT chest images	Ffit_4	337	365
	SARS-COV-2 CT-scan images	Ffit_5	621	1166
	coronavirus CT scan images	Ffit_6	61	80

TABLE 2: DATASET PORTIONING

Feature Fitting Data	coronavirus				Non- coronavirus			
	Training	Validation	Testing	Total	Training	Validation	Testing	Total
Ffit_1	720	146	145	1011	912	198	198	1308
Ffit_2	948	210	234	1392	470	159	160	789
Ffit_3	155	32	36	223	156	39	37	232
Ffit_4	245	43	49	337	265	51	49	365
Ffit_5	389	102	130	621	689	210	267	1166
Ffit_6	34	15	12	61	49	19	12	80

This research work developed an AI-based CoV19 feature prediction model, which has been tested with original and data-augmented datasets. All the scan images are resized based on the feature size of 256x256 pixels with a change in aspect ratio, compare to the original.

Fig. 2(A) and **(B)** illustrate the chest X-ray images of CoV-19 infected and healthy patients, respectively. The CoV19 detection model is a

combination of the proposed model FVisL-CoV19 and VGG16, through AI and they are used to detect CoV19 using chest X-ray and CT scan images.

Fig. 2(C) and **(D)** illustrate the CT scan images of CoV-19 infected and healthy patients, respectively. The collected chest X-rays and CT scans were split into a training data subset and a testing data subset, illustrated in **Table 2**.

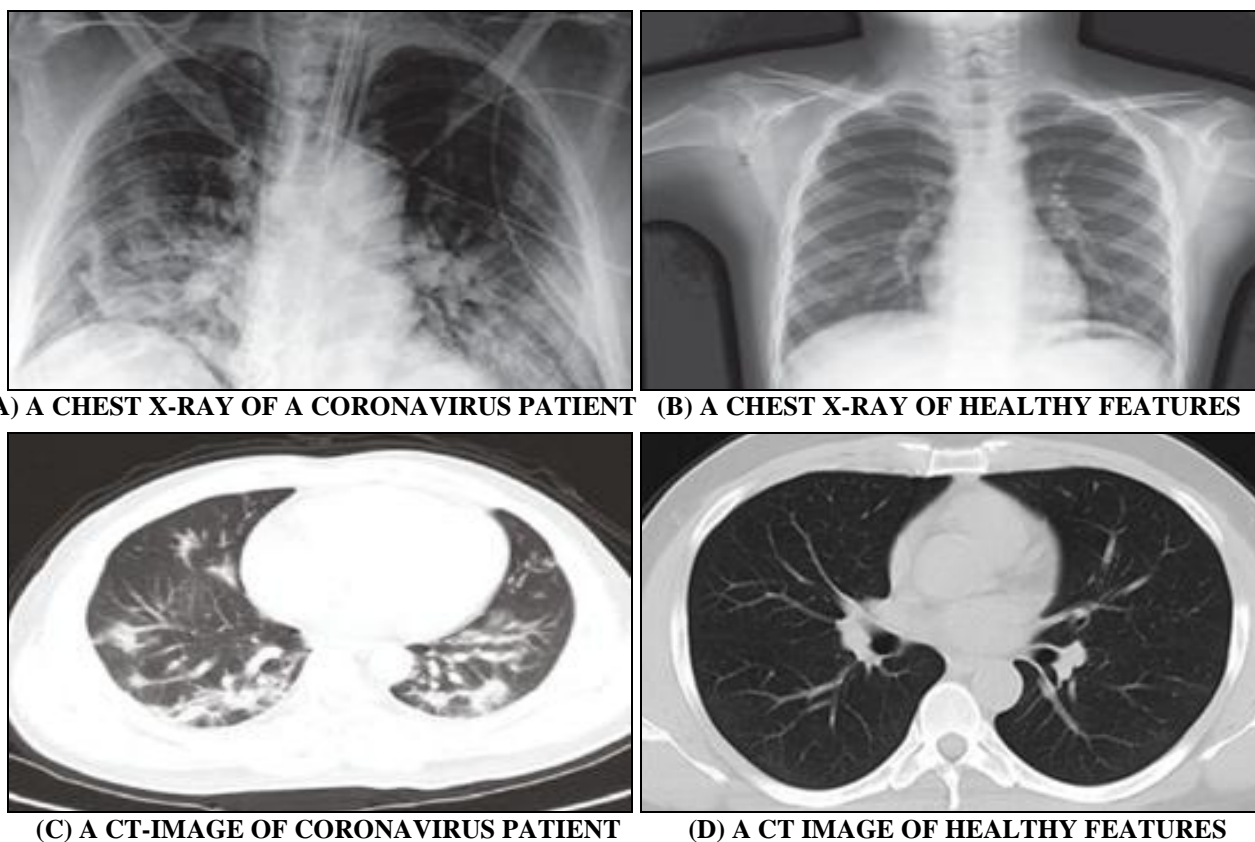


FIG. 2: SAMPLE OF THE COVID-19 DATASET

Fig. 3 illustrates the feature validations of the original scan image considered for the proposed model analysis, 3 (a) shows the original scan image showing the features region (outlined in green color) to the model, 3 (b) shows the pixels distribution before features validation showing the artifacts of the features analyzed during the initial stage of the diagnosis process, 3 (c) shows the features region enhanced for the model from original scan image showing the improved diagnosis collected data where the infected human being is identified with feature-level collected data, and 3 (d) shows the pixels distribution after features validation showing the identified artifacts of infection, which were corrected after feature-

level extraction. **Fig. 4** illustrates the working of the AI structural model, 4 (a) visualizes the feature region considered for structuring the model, 4 (b) the input layer shows the analysis in identifying the location of infection regions, 4 (c) hidden layer shows the changes in symptoms infection analysis in estimating the infection status based on the region of human being movement, 4 (d) output layer shows the contact feature tracing by estimating the infection progression through contact, and 4 (e) Visualization of AI diagnosis features map shows the infection confirm status from the scan and visual features through infection diagnose.

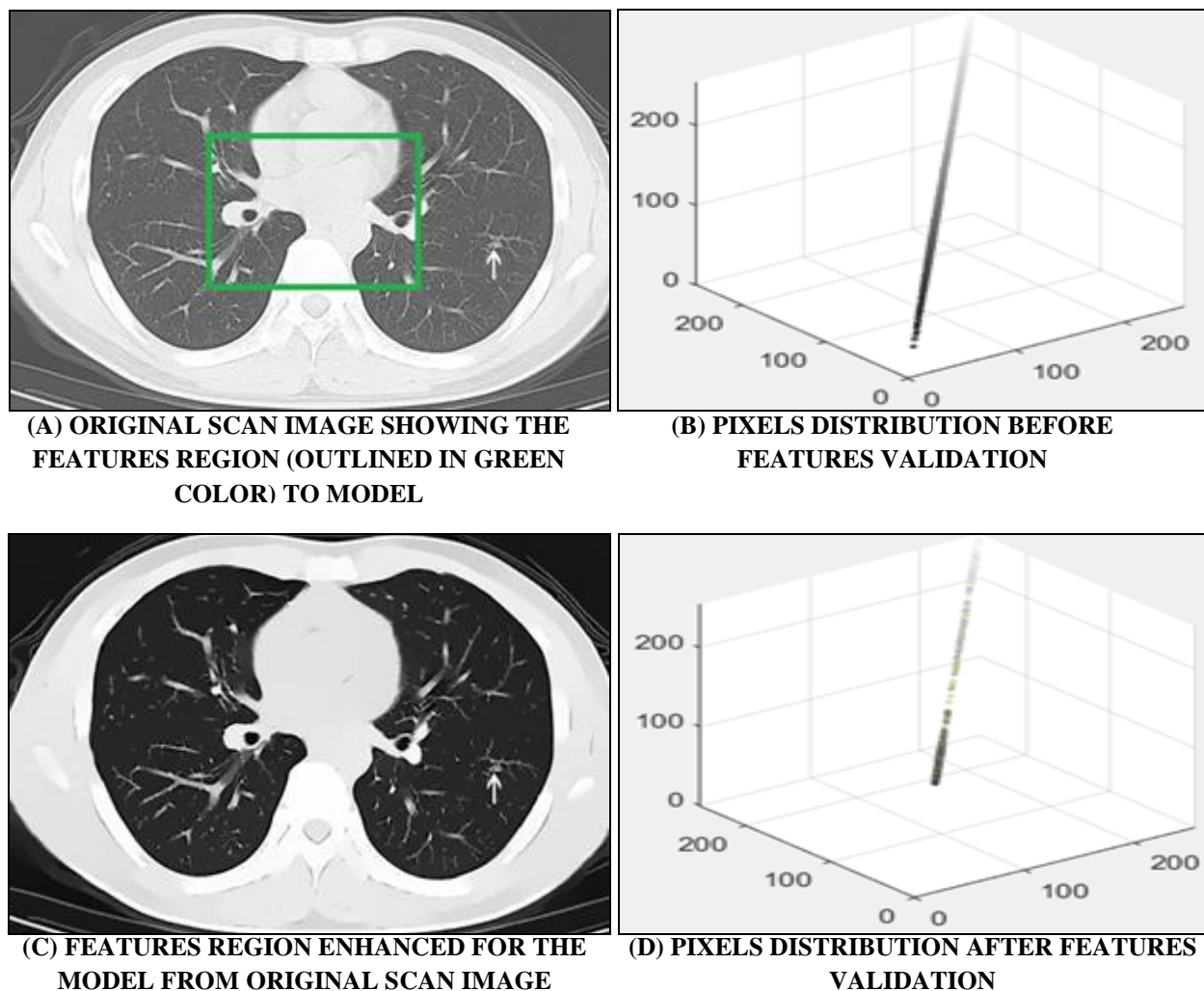
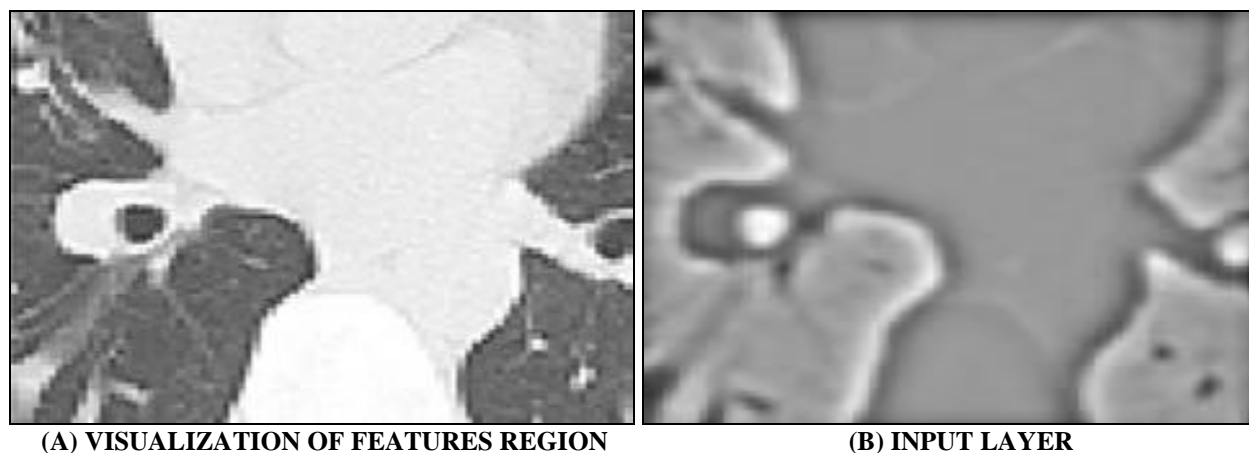
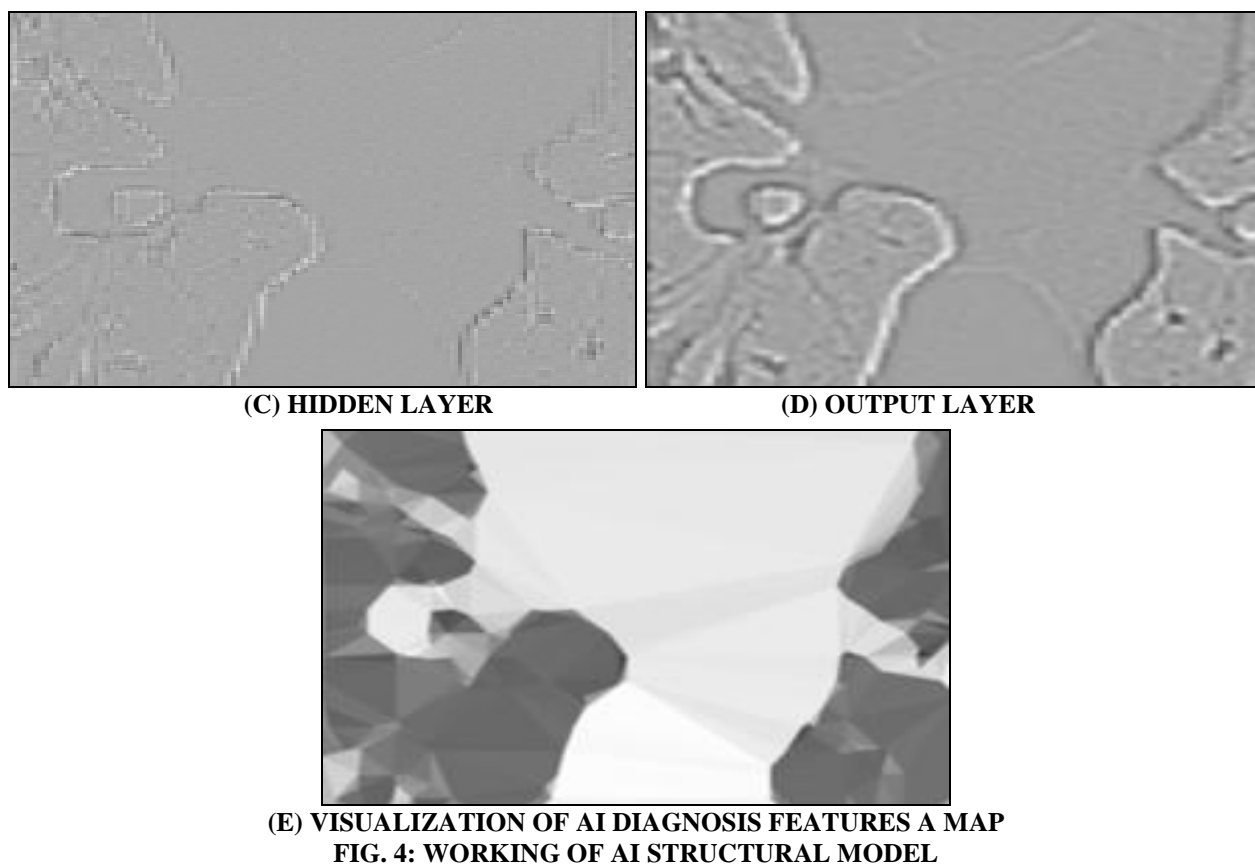


FIG. 3: FEATURE VALIDATIONS

Fig. 4 illustrates the working of the AI structural model, 4 (a) visualizes the feature region considered for structuring the model, 4 (b) the input layer shows the analysis in identifying the location of infection regions, 4 (c) hidden layer shows the changes in symptoms infection analysis in estimating the infection status based on the region

of human being movement, 4 (d) output layer shows the contact feature tracing by estimating the infection progression through contact and 4 (e) Visualization of AI diagnosis features map shows the infection confirm status from the scan and visual features through infection diagnose.





Performance Evaluation: The proposed model is to identify CoV19 and non-CoV19 samples based on the performance metrics illustrated in **Table 3**, Prediction metrics.

TABLE 3: PERFORMANCE METRIC FOR PREDICTION

Performance metric	Definition
TN as True Negative	Correctly identified as Negative
TP as True Positive	Correctly identified as Positive
FN as False Negative	Incorrectly identified as Negative
FP as False Positive	Incorrectly identified as Positive

Based on **Table 3**, the evaluation metrics formulae are illustrated in **Table 4**.

TABLE 4: EVALUATION METRICS

Evaluation metric	Definition
Accuracy (in %) (A)	$TP + TN / TP + FP + TN + FN$
Precision (in %) (P)	$TP / TP + FP$
Recall (R)	$TP / TP + FN$
F1 score (F1)	$2 \times R \times P / R + P$

TABLE 5: PERFORMANCE EVALUATION OF THE PROPOSED AND PREVIOUS MODELS

Method	Precision	Recall	F1-Score	Accuracy
DensNet [37]	98.3	96	97.1	96.7
3D-UNet[38]	97.4	91.5	97.9	97.9
Proposed model	98.3	98.6	98.5	98.4

Table 5 illustrates the performance of the proposed model and previously published models for a common COVID-19 dataset. It is observed that the proposed model achieves better recall to detect COVID-19-infected images because it has feature texture analysis parameters to distinguish the feature classes. And the proposed model has better accuracy in analyzing the features by classifying the dataset accordingly to identify the symptoms patterns.

CONCLUSIONS: The proposed work uses the public coronavirus dataset to model an effective coronavirus infection diagnosis system. The important design of the model proposed is current AI incorporates a structural model design construction to enhance the infection feature analysis for the original scan images and real-time human being movement, having infected, moderate-infected, and non-infected forms of multi-layer extractions. Comparatively, the accuracy of the proposed model is analyzed with coronavirus and normal scan image datasets. The proposed model experiment results show better accuracy and can achieve a better infection features diagnosis model better than other models.

In the future, this model can be used to analyze coronavirus infections with identified factors of trained infected scans, based on model parameters defined in this research work.

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CONFLICTS OF INTEREST: Nil

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